



SEQUENCE LISTING

<110> Presnell, Scott R.
Burkhead, Steven K.
Powder, Sarah L.

<120> Human Cytokine Receptor

<130> 99-50

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<170> FastSEQ for Windows Version 3.0

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<212> DNA

<213> Homo sapiens

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cctcaggcct gggtgccacc tggcacctag aag atg cct gtg ccc tgg ttc ttg 174
Met Pro Val Pro Trp Phe Leu
1 5

ctg tcc ttg gca ctg ggc cga agc cca gtg gtc ctt tct ctg gag agg 222
Leu Ser Leu Ala Leu Gly Arg Ser Pro Val Val Leu Ser Leu Glu Arg
10 15 20

ctt gtg ggg cct cag gac gct acc cac tgc tct ccg ggc ctc tcc tgc 270
Leu Val Gly Pro Gln Asp Ala Thr His Cys Ser Pro Gly Leu Ser Cys
25 30 35

cgc ctc tgg gac agt gac ata ctc tgc ctg cct ggg gac atc gtg cct 318
Arg Leu Trp Asp Ser Asp Ile Leu Cys Leu Pro Gly Asp Ile Val Pro
40 45 50 55

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AI

gct ccg ggc ccc gtg ctg gcg cct acg cac ctg cag aca gag ctg gtg 366
Ala Pro Gly Pro Val Leu Ala Pro Thr His Leu Gln Thr Glu Leu Val
60 65 70

ctg agg tgc cag aag gag acc gac tgt gac ctg tgt ctg cgt gtg gct 414
Leu Arg Cys Gln Lys Glu Thr Asp Cys Asp Leu Cys Leu Arg Val Ala
75 80 85

gtc cac ttg gcc gtg cat ggg cac tgg gaa gag cct gaa gat gag gaa 462
Val His Leu Ala Val His Gly His Trp Glu Glu Pro Glu Asp Glu Glu
90 95 100

aag ttt gga gga gca gct gac tca ggg gtg gag gag cct agg aat gcc 510
Lys Phe Gly Gly Ala Ala Asp Ser Gly Val Glu Glu Pro Arg Asn Ala
105 110 115

tct ctg cag gcc caa gtc gtg ctg tcc ttc cag gcc tac cct act gcc 558
Ser Leu Gln Ala Gln Val Val Leu Ser Phe Gln Ala Tyr Pro Thr Ala
120 125 130 135

cgc tgc gtc ctg ctg gag gtg caa gtg cct gct gcc ctt gtg cag ttt 606
Arg Cys Val Leu Leu Glu Val Gln Val Pro Ala Ala Leu Val Gln Phe
140 145 150

ggc cag tct gtg ggc tct gtg gta tat gac tgc ttc gag gct gcc cta 654
Gly Gln Ser Val Gly Ser Val Val Tyr Asp Cys Phe Glu Ala Ala Leu
155 160 165

ggg agt gag gta cga atc tgg tcc tat act cag ccc agg tac gag aag 702
Gly Ser Glu Val Arg Ile Trp Ser Tyr Thr Gln Pro Arg Tyr Glu Lys
170 175 180

gaa ctg aac cac aca cag cag ctg cct gcc ctg ccc tgg ctg aac gtg 750
Glu Leu Asn His Thr Gln Gln Leu Pro Ala Leu Pro Trp Leu Asn Val
185 190 195

tca gca gat ggt gac aac gtg cat ctg gtt ctg aat gtc tct gag gag 798
Ser Ala Asp Gly Asp Asn Val His Leu Val Leu Asn Val Ser Glu Glu
200 205 210 215

cag cac ttc ggc ctg tcc ctg tac tgg aat cag gtc cag ggc ccc cca 846
Gln His Phe Gly Leu Ser Leu Tyr Trp Asn Gln Val Gln Gly Pro Pro
220 225 230

AI
cont.

aaa ccc cgg tgg cac aaa aac ctg act gga ccg cag atc att acc ttg 894
 Lys Pro Arg Trp His Lys Asn Leu Thr Gly Pro Gln Ile Ile Thr Leu
 235 240 245

aac cac aca gac ctg gtt ccc tgc ctc tgt att cag gtg tgg cct ctg 942
 Asn His Thr Asp Leu Val Pro Cys Leu Cys Ile Gln Val Trp Pro Leu
 250 255 260

gaa cct gac tcc gtt agg acg aac atc tgc ccc ttc agg gag gac ccc 990
 Glu Pro Asp Ser Val Arg Thr Asn Ile Cys Pro Phe Arg Glu Asp Pro
 265 270 275

cgc gca cac cag aac ctc tgg caa gcc gcc cga ctg cga ctg ctg acc 1038
 Arg Ala His Gln Asn Leu Trp Gln Ala Ala Arg Leu Arg Leu Leu Thr
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ctg cag agc tgg ctg ctg gac gca ccg tgc tcg ctg ccc gca gaa gcg 1086
 Leu Gln Ser Trp Leu Leu Asp Ala Pro Cys Ser Leu Pro Ala Glu Ala
 300 305 310

gca ctg tgc tgg cgg gct ccg ggt ggg gac ccc tgc cag cca ctg gtc 1134
 Ala Leu Cys Trp Arg Ala Pro Gly Gly Asp Pro Cys Gln Pro Leu Val
 315 320 325

cca ccg ctt tcc tgg gag aac gtc act gtg gac aag gtt ctc gag ttc 1182
 Pro Pro Leu Ser Trp Glu Asn Val Thr Val Asp Lys Val Leu Glu Phe
 330 335 340

cca ttg ctg aaa ggc cac cct aac ctc tgt gtt cag gtg aac agc tcg 1230
 Pro Leu Leu Lys Gly His Pro Asn Leu Cys Val Gln Val Asn Ser Ser
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 Glu Lys Leu Gln Leu Gln Glu Cys Leu Trp Ala Asp Ser Leu Gly Pro
 360 365 370 375

ctc aaa gac gat gtg cta ctg ttg gag aca cga ggc ccc cag gac aac 1326
 Leu Lys Asp Asp Val Leu Leu Leu Glu Thr Arg Gly Pro Gln Asp Asn
 380 385 390

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A1
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395 400 405	
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Lys Ala Ser Thr Arg Ala Ala Arg Leu Gly Glu Tyr Leu Leu Gln Asp	
410 415 420	
ctg cag tca ggc cag tgt ctg cag cta tgg gac gat gac ttg gga gcg	1470
Leu Gln Ser Gly Gln Cys Leu Gln Leu Trp Asp Asp Asp Leu Gly Ala	
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cta tgg gcc tgc ccc atg gac aaa tac atc cac aag cgc tgg gcc ctc	1518
Leu Trp Ala Cys Pro Met Asp Lys Tyr Ile His Lys Arg Trp Ala Leu	
440 445 450 455	
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Val Trp Leu Ala Cys Leu Leu Phe Ala Ala Ala Leu Ser Leu Ile Leu	
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Leu Leu Lys Lys Asp His Ala Lys Ala Ala Ala Arg Gly Arg Ala Ala	
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Leu Leu Leu Tyr Ser Ala Asp Asp Ser Gly Phe Glu Arg Leu Val Gly	
490 495 500	
gcc ctg gcg tcg gcc ctg tgc cag ctg ccg ctg cgc gtg gcc gta gac	1710
Ala Leu Ala Ser Ala Leu Cys Gln Leu Pro Leu Arg Val Ala Val Asp	
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His Ala Gln Arg Arg Gln Thr Leu Gln Glu Gly Gly Val Val Val Leu	
540 545 550	
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555 560 565	

Val Val Leu Ser Leu Glu Arg Leu Val Gly Pro Gln Asp Ala Thr His
 20 25 30
 Cys Ser Pro Gly Leu Ser Cys Arg Leu Trp Asp Ser Asp Ile Leu Cys
 35 40 45
 Leu Pro Gly Asp Ile Val Pro Ala Pro Gly Pro Val Leu Ala Pro Thr
 50 55 60
 His Leu Gln Thr Glu Leu Val Leu Arg Cys Gln Lys Glu Thr Asp Cys
 65 70 75 80
 Asp Leu Cys Leu Arg Val Ala Val His Leu Ala Val His Gly His Trp
 85 90 95
 Glu Glu Pro Glu Asp Glu Glu Lys Phe Gly Gly Ala Ala Asp Ser Gly
 100 105 110
 Val Glu Glu Pro Arg Asn Ala Ser Leu Gln Ala Gln Val Val Leu Ser
 115 120 125
 Phe Gln Ala Tyr Pro Thr Ala Arg Cys Val Leu Leu Glu Val Gln Val
 130 135 140
 Pro Ala Ala Leu Val Gln Phe Gly Gln Ser Val Gly Ser Val Val Tyr
 145 150 155 160
 Asp Cys Phe Glu Ala Ala Leu Gly Ser Glu Val Arg Ile Trp Ser Tyr
 165 170 175
 Thr Gln Pro Arg Tyr Glu Lys Glu Leu Asn His Thr Gln Gln Leu Pro
 180 185 190
 Ala Leu Pro Trp Leu Asn Val Ser Ala Asp Gly Asp Asn Val His Leu
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 Val Leu Asn Val Ser Glu Glu Gln His Phe Gly Leu Ser Leu Tyr Trp
 210 215 220
 Asn Gln Val Gln Gly Pro Pro Lys Pro Arg Trp His Lys Asn Leu Thr
 225 230 235 240
 Gly Pro Gln Ile Ile Thr Leu Asn His Thr Asp Leu Val Pro Cys Leu
 245 250 255
 Cys Ile Gln Val Trp Pro Leu Glu Pro Asp Ser Val Arg Thr Asn Ile
 260 265 270
 Cys Pro Phe Arg Glu Asp Pro Arg Ala His Gln Asn Leu Trp Gln Ala
 275 280 285
 Ala Arg Leu Arg Leu Leu Thr Leu Gln Ser Trp Leu Leu Asp Ala Pro
 290 295 300
 Cys Ser Leu Pro Ala Glu Ala Ala Leu Cys Trp Arg Ala Pro Gly Gly
 305 310 315 320
 Asp Pro Cys Gln Pro Leu Val Pro Pro Leu Ser Trp Glu Asn Val Thr
 325 330 335
 Val Asp Lys Val Leu Glu Phe Pro Leu Leu Lys Gly His Pro Asn Leu
 340 345 350

Cys Val Gln Val Asn Ser Ser Glu Lys Leu Gln Leu Gln Glu Cys Leu
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 Trp Ala Asp Ser Leu Gly Pro Leu Lys Asp Asp Val Leu Leu Leu Glu
 370 375 380
 Thr Arg Gly Pro Gln Asp Asn Arg Ser Leu Cys Ala Leu Glu Pro Ser
 385 390 395 400
 Gly Cys Thr Ser Leu Pro Ser Lys Ala Ser Thr Arg Ala Ala Arg Leu
 405 410 415
 Gly Glu Tyr Leu Leu Gln Asp Leu Gln Ser Gly Gln Cys Leu Gln Leu
 420 425 430
 Trp Asp Asp Asp Leu Gly Ala Leu Trp Ala Cys Pro Met Asp Lys Tyr
 435 440 445
 Ile His Lys Arg Trp Ala Leu Val Trp Leu Ala Cys Leu Leu Phe Ala
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 Ala Ala Leu Ser Leu Ile Leu Leu Leu Lys Lys Asp His Ala Lys Ala
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 Pro Leu Arg Val Ala Val Asp Leu Trp Ser Arg Arg Glu Leu Ser Ala
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 Gln Gly Pro Val Ala Trp Phe His Ala Gln Arg Arg Gln Thr Leu Gln
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 Glu Gly Gly Val Val Val Leu Leu Phe Ser Pro Gly Ala Val Ala Leu
 545 550 555 560
 Cys Ser Glu Trp Leu Gln Asp Gly Val Ser Gly Pro Gly Ala His Gly
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 Pro His Asp Ala Phe Arg Ala Ser Leu Ser Cys Val Leu Pro Asp Phe
 580 585 590
 Leu Gln Gly Arg Ala Pro Gly Ser Tyr Val Gly Ala Cys Phe Asp Arg
 595 600 605
 Leu Leu His Pro Asp Ala Val Pro Ala Leu Phe Arg Thr Val Pro Val
 610 615 620
 Phe Thr Leu Pro Ser Gln Leu Pro Asp Phe Leu Gly Ala Leu Gln Gln
 625 630 635 640
 Pro Arg Ala Pro Arg Ser Gly Arg Leu Gln Glu Arg Ala Glu Gln Val
 645 650 655
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Gly Asp Gly Thr
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sequence of SEQ ID NO:2.

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<223> N is any nucleotide

<221> misc_feature
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gayytntggy	tnmgngtngc	ngtncayyt	gcngtncayg	gncaytggga	rgarccngar	300
gaygargara	arttyggngg	ngcngcngay	wsnggngtng	argarccnmg	naaygcnwsn	360
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gargtncarg	tnccngcngc	nytngtncar	ttyggncarw	sngtnggnws	ngtngtntay	480
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acngtnccng tnttyacnyt nccnwsncar ytnccngayt tyytnggngc nytnccar	1920
ccnmngngcnc cnmgnwsngg nmgnytncar garmngngcng arcargtnws nmngngcnytn	1980
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Gln Ala Tyr Pro Thr Ala Arg Cys Val Leu Leu Glu Val Gln Val Pro	
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gct gcc ctt gtg cag ttt ggt cag tct gtg ggc tct gtg gta tat gac	145
Ala Ala Leu Val Gln Phe Gly Gln Ser Val Gly Ser Val Val Tyr Asp	
35 40 45	

tgc ttc gag gct gcc cta ggg agt gag gta cga atc tgg tcc tat act	193
Cys Phe Glu Ala Ala Leu Gly Ser Glu Val Arg Ile Trp Ser Tyr Thr	
50 55 60	

cag ccc agg tac gag aag gaa ctc aac cac aca cag cag ctg cct gcc	241
Gln Pro Arg Tyr Glu Lys Glu Leu Asn His Thr Gln Gln Leu Pro Ala	
65 70 75 80	

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cag gtc cag ggc ccc cca aaa ccc cgg tgg cac aaa aac ctg act gga Gln Val Gln Gly Pro Pro Lys Pro Arg Trp His Lys Asn Leu Thr Gly 115 120 125	385
ccg cag atc att acc ttg aac cac aca gac ctg gtt ccc tgc ctc tgt Pro Gln Ile Ile Thr Leu Asn His Thr Asp Leu Val Pro Cys Leu Cys 130 135 140	433
att cag gtg tgg cct ctg gaa cct gac tcc gtt agg acg aac atc tgc Ile Gln Val Trp Pro Leu Glu Pro Asp Ser Val Arg Thr Asn Ile Cys 145 150 155 160	481
ccc ttc agg gag gac ccc cgc gca cac cag aac ctc tgg caa gcc gcc Pro Phe Arg Glu Asp Pro Arg Ala His Gln Asn Leu Trp Gln Ala Ala 165 170 175	529
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tcg ctg ccc gca gaa gcg gca ctg tgc tgg cgg gct ccg ggt ggg gac Ser Leu Pro Ala Glu Ala Ala Leu Cys Trp Arg Ala Pro Gly Gly Asp 195 200 205	625
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gac gtg aac agc tcg gag aag ctg cag ctg cag gag tgc ttg tgg gct Asp Val Asn Ser Ser Glu Lys Leu Gln Leu Gln Glu Cys Leu Trp Ala 225 230 235 240	721
gac tcc ctg ggg cct ctc aaa gac gat gtg cta ctg ttg gag aca cga	769

Asp Ser Leu Gly Pro Leu Lys Asp Asp Val Leu Leu Leu Glu Thr Arg	
245 250 255	
ggc ccc cag gac aac aga tcc ctc tgt gcc ttg gaa ccc agt ggc tgt	817
Gly Pro Gln Asp Asn Arg Ser Leu Cys Ala Leu Glu Pro Ser Gly Cys	
260 265 270	
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Thr Ser Leu Pro Ser Lys Ala Ser Thr Arg Ala Ala Arg Leu Gly Glu	
275 280 285	
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Tyr Leu Leu Gln Asp Leu Gln Ser Gly Gln Cys Leu Gln Leu Trp Asp	
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Asp Asp Leu Gly Ala Leu Trp Ala Cys Pro Met Asp Lys Tyr Ile His	
305 310 315 320	
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Lys Arg Trp Ala Leu Val Trp Leu Ala Cys Leu Leu Phe Ala Ala Ala	
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ctt tcc ctc atc ctc ctt ctc aaa aag gat cac gcg aaa ggg tgg ctg	1057
Leu Ser Leu Ile Leu Leu Leu Lys Lys Asp His Ala Lys Gly Trp Leu	
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gcg gct ctg ctc ctc tac tca gcc gat gac tcg ggt ttc gag cgc ctg	1153
Ala Ala Leu Leu Leu Tyr Ser Ala Asp Asp Ser Gly Phe Glu Arg Leu	
370 375 380	
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Val Gly Ala Leu Ala Ser Ala Leu Cys Gln Leu Pro Leu Arg Val Ala	
385 390 395 400	
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Val Asp Leu Trp Ser Arg Arg Glu Leu Ser Ala Gln Gly Pro Val Ala	
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Trp Phe His Ala Gln Arg Arg Gln Thr Leu Gln Glu Gly Gly Val Val	
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Gln Asp Gly Val Ser Gly Pro Gly Ala His Gly Pro His Asp Ala Phe	
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Arg Ala Ser Leu Ser Cys Val Leu Pro Asp Phe Leu Gln Gly Arg Ala	
465 470 475 480	
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Pro Gly Ser Tyr Val Gly Ala Cys Phe Asp Arg Leu Leu His Pro Asp	
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Gln Leu Pro Asp Phe Leu Gly Ala Leu Gln Gln Pro Arg Ala Pro Arg	
515 520 525	
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Pro Ala Leu Asp Ser Tyr Phe His Pro Pro Gly Thr Pro Ala Pro Gly	
545 550 555 560	
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<211> 575
 <212> PRT
 <213> Homo sapiens

<400> 5

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Ala	Ala	Leu	Val	Gln	Phe	Gly	Gln	Ser	Val	Gly	Ser	Val	Val	Tyr	Asp
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Cys	Phe	Glu	Ala	Ala	Leu	Gly	Ser	Glu	Val	Arg	Ile	Trp	Ser	Tyr	Thr
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Gln	Pro	Arg	Tyr	Glu	Lys	Glu	Leu	Asn	His	Thr	Gln	Gln	Leu	Pro	Ala
65					70					75				80	
Leu	Pro	Trp	Leu	Asn	Val	Ser	Ala	Asp	Gly	Asp	Asn	Val	His	Leu	Val
			85						90					95	
Leu	Asn	Val	Ser	Glu	Glu	Gln	His	Phe	Gly	Leu	Ser	Leu	Tyr	Trp	Asn
			100						105				110		
Gln	Val	Gln	Gly	Pro	Pro	Lys	Pro	Arg	Trp	His	Lys	Asn	Leu	Thr	Gly
		115					120					125			
Pro	Gln	Ile	Ile	Thr	Leu	Asn	His	Thr	Asp	Leu	Val	Pro	Cys	Leu	Cys
	130					135					140				
Ile	Gln	Val	Trp	Pro	Leu	Glu	Pro	Asp	Ser	Val	Arg	Thr	Asn	Ile	Cys
145					150					155				160	
Pro	Phe	Arg	Glu	Asp	Pro	Arg	Ala	His	Gln	Asn	Leu	Trp	Gln	Ala	Ala
			165						170					175	
Arg	Leu	Arg	Leu	Leu	Thr	Leu	Gln	Ser	Trp	Leu	Leu	Asp	Ala	Pro	Cys
			180					185					190		
Ser	Leu	Pro	Ala	Glu	Ala	Ala	Leu	Cys	Trp	Arg	Ala	Pro	Gly	Gly	Asp
		195					200					205			
Pro	Cys	Gln	Pro	Leu	Val	Pro	Pro	Leu	Ser	Trp	Glu	Asn	Val	Thr	Val
	210					215					220				
Asp	Val	Asn	Ser	Ser	Glu	Lys	Leu	Gln	Leu	Gln	Glu	Cys	Leu	Trp	Ala
225					230					235				240	
Asp	Ser	Leu	Gly	Pro	Leu	Lys	Asp	Asp	Val	Leu	Leu	Leu	Glu	Thr	Arg
			245						250					255	
Gly	Pro	Gln	Asp	Asn	Arg	Ser	Leu	Cys	Ala	Leu	Glu	Pro	Ser	Gly	Cys
		260					265						270		
Thr	Ser	Leu	Pro	Ser	Lys	Ala	Ser	Thr	Arg	Ala	Ala	Arg	Leu	Gly	Glu
		275					280					285			
Tyr	Leu	Leu	Gln	Asp	Leu	Gln	Ser	Gly	Gln	Cys	Leu	Gln	Leu	Trp	Asp
	290					295						300			

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Asp Asp Leu Gly Ala Leu Trp Ala Cys Pro Met Asp Lys Tyr Ile His
305          310          315          320
Lys Arg Trp Ala Leu Val Trp Leu Ala Cys Leu Leu Phe Ala Ala Ala
          325          330          335
Leu Ser Leu Ile Leu Leu Leu Lys Lys Asp His Ala Lys Gly Trp Leu
          340          345          350
Arg Leu Leu Lys Gln Asp Val Arg Ser Gly Ala Ala Ala Arg Gly Arg
          355          360          365
Ala Ala Leu Leu Leu Tyr Ser Ala Asp Asp Ser Gly Phe Glu Arg Leu
          370          375          380
Val Gly Ala Leu Ala Ser Ala Leu Cys Gln Leu Pro Leu Arg Val Ala
385          390          395          400
Val Asp Leu Trp Ser Arg Arg Glu Leu Ser Ala Gln Gly Pro Val Ala
          405          410          415
Trp Phe His Ala Gln Arg Arg Gln Thr Leu Gln Glu Gly Gly Val Val
          420          425          430
Val Leu Leu Phe Ser Pro Gly Ala Val Ala Leu Cys Ser Glu Trp Leu
          435          440          445
Gln Asp Gly Val Ser Gly Pro Gly Ala His Gly Pro His Asp Ala Phe
          450          455          460
Arg Ala Ser Leu Ser Cys Val Leu Pro Asp Phe Leu Gln Gly Arg Ala
465          470          475          480
Pro Gly Ser Tyr Val Gly Ala Cys Phe Asp Arg Leu Leu His Pro Asp
          485          490          495
Ala Val Pro Ala Leu Phe Arg Thr Val Pro Val Phe Thr Leu Pro Ser
          500          505          510
Gln Leu Pro Asp Phe Leu Gly Ala Leu Gln Gln Pro Arg Ala Pro Arg
          515          520          525
Ser Gly Arg Leu Gln Glu Arg Ala Glu Gln Val Ser Arg Ala Leu Gln
          530          535          540
Pro Ala Leu Asp Ser Tyr Phe His Pro Pro Gly Thr Pro Ala Pro Gly
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Arg Gly Val Gly Pro Gly Ala Gly Pro Gly Ala Gly Asp Gly Thr
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<210> 6

<211> 1725

<212> DNA

<213> Artificial Sequence

<220>

<223> This degenerate sequence encodes the amino acid
sequence of SEQ ID NO:5.

<221> variation
 <222> (1)...(1725)
 <223> N is any nucleotide.

<221> misc_feature
 <222> (1)...(1725)
 <223> n = A,T,C or G

<400> 6

AI
 conf.

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acngcnmgnt	gygtntytyt	ngargtnear	gtncngcng	cnytngtnc	rttyggncar	120
wsngtnggnw	sngtngtnta	ygaytgytty	gargcngcny	tnggnwsnga	rgtnmgnath	180
tggwsntaya	cncarccnmg	ntaygaraar	garytnaayc	ayacncarca	rytnccngcn	240
ytnccntggy	tnaaygtnws	ngcngayggn	gayaaygtnc	ayytngtnyt	naaygtnwsn	300
gargarcarc	ayttyggnyt	nwsnytnay	tggaaycarg	tncarggncc	nccnaarccn	360
mgntggcaya	araayytnac	nggnccncar	athathacny	tnaaycayac	ngayytngtn	420
ccntggytnt	gyathcargt	ntggccnytn	garccngayw	sngtnmgnac	naayathtgy	480
ccnttymgng	argayccnmg	ngcncaycar	aayytntggc	argcngcnmg	nytnmgnytn	540
ytnacnytn	arwsntggyt	nytnngaycn	ccntgywsny	tnccngcnga	rgcngcnytn	600
tgytggmgng	cncngngng	ngayccntgy	carccnytn	tnccncnytn	nwsntgggar	660
aaygtnacng	tngaygtnaa	ywsnwsngar	aarytnary	tncargartg	yytntgggcn	720
gaywsnytn	gncnytnaa	rgaygaygt	ytnytnytn	aracnmngng	nccncargay	780
aaymgnwsny	tntgygcny	ngarccnwsn	ggntgyacnw	snytnccnws	naargcnwsn	840
acnmngcng	cnmgnytn	ngartayytn	ytnccargay	tnccarwsng	ncartgyytn	900
carytntggy	aygaygayt	nggngcnytn	tgggcntgyc	cnatggayaa	rtayathcay	960
aarmgntggg	cnytngtntg	gytnccntgy	ytnytnntyg	cngcngcnytn	nwsnytnath	1020
ytnytnytna	araargayca	ygcnaarggn	tggynmngny	tnytnaarca	rgaygtnmgn	1080
wsnggngcng	cngcnmgng	nmngngcng	ytnytnytn	aywsngcnga	ygaywsnggn	1140
ttygarmgny	tngtngngc	nytnccnwsn	gcnytnntyg	arytnccnytn	nmngntngcn	1200
gtngayytn	ggwsnmngm	ngarytnwsn	gcncarggnc	cngtngcntg	gttycaygc	1260
carmgngnc	aracnytna	rgarggnggn	gtngtngtny	tnytnnttyws	nccnggngcn	1320
gtngcnytn	gywsngartg	gytnccargay	ggngtnwsng	gnccnggngc	ncayggncn	1380
caygaygcnt	tymngncnws	nytnwsntgy	gtnytnccng	ayttyytna	rggnmgngcn	1440
ccnggnwsnt	aygtngngc	ntgyttygay	mgnytnytn	ayccngaygc	ngtnccngcn	1500
ytnntymgna	cngtnccngt	nttyacnytn	ccnwsncary	tnccngaytt	yytnngngcn	1560
ytnccarcarc	cnmgngcnc	nmgnwsnggn	mgnytnccarg	armgngcnga	rcargtnwsn	1620
mgngcnytn	arccngcnytn	ngaywsntay	ttycayccnc	cnggnacncc	ngcncnggn	1680
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<213> Artificial Sequence

<220>

<223> Peptide linker.

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<210> 8

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

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cggcgtggtg gtcttgctct t

21

<210> 9

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer.

<400> 9

tcccgtcccc cgccccaggt c

21

<210> 10

<211> 688

<212> PRT

<213> Artificial Sequence

<220>

<223> Chimeric Zcytor14 protein.

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1 5 10 15

Val	Val	Leu	Ser	Leu	Glu	Arg	Leu	Val	Gly	Pro	Gln	Asp	Ala	Thr	His
		20						25					30		
Cys	Ser	Pro	Gly	Leu	Ser	Cys	Arg	Leu	Trp	Asp	Ser	Asp	Ile	Leu	Cys
		35					40					45			
Leu	Pro	Gly	Asp	Ile	Val	Pro	Ala	Pro	Gly	Pro	Val	Leu	Ala	Pro	Thr
	50					55					60				
His	Leu	Gln	Thr	Glu	Leu	Val	Leu	Arg	Cys	Gln	Lys	Glu	Thr	Asp	Cys
65					70					75				80	
Asp	Leu	Cys	Leu	Arg	Val	Ala	Val	His	Leu	Ala	Val	His	Gly	His	Trp
				85					90					95	
Glu	Glu	Pro	Glu	Asp	Glu	Glu	Lys	Phe	Gly	Gly	Ala	Ala	Asp	Ser	Gly
			100					105					110		
Val	Glu	Glu	Pro	Arg	Asn	Ala	Ser	Leu	Gln	Ala	Gln	Val	Val	Leu	Ser
		115					120					125			
Phe	Gln	Ala	Tyr	Pro	Thr	Ala	Arg	Cys	Val	Leu	Leu	Glu	Val	Gln	Val
	130					135						140			
Pro	Ala	Ala	Leu	Val	Gln	Phe	Gly	Gln	Ser	Val	Gly	Ser	Val	Val	Tyr
145					150					155					160
Asp	Cys	Phe	Glu	Ala	Ala	Leu	Gly	Ser	Glu	Val	Arg	Ile	Trp	Ser	Tyr
				165					170					175	
Thr	Gln	Pro	Arg	Tyr	Glu	Lys	Glu	Leu	Asn	His	Thr	Gln	Gln	Leu	Pro
		180						185						190	
Ala	Leu	Pro	Trp	Leu	Asn	Val	Ser	Ala	Asp	Gly	Asp	Asn	Val	His	Leu
		195					200					205			
Val	Leu	Asn	Val	Ser	Glu	Glu	Gln	His	Phe	Gly	Leu	Ser	Leu	Tyr	Trp
	210					215					220				
Asn	Gln	Val	Gln	Gly	Pro	Pro	Lys	Pro	Arg	Trp	His	Lys	Asn	Leu	Thr
225					230					235					240
Gly	Pro	Gln	Ile	Ile	Thr	Leu	Asn	His	Thr	Asp	Leu	Val	Pro	Cys	Leu
				245					250					255	
Cys	Ile	Gln	Val	Trp	Pro	Leu	Glu	Pro	Asp	Ser	Val	Arg	Thr	Asn	Ile
		260						265					270		
Cys	Pro	Phe	Arg	Glu	Asp	Pro	Arg	Ala	His	Gln	Asn	Leu	Trp	Gln	Ala
		275					280					285			
Ala	Arg	Leu	Arg	Leu	Leu	Thr	Leu	Gln	Ser	Trp	Leu	Leu	Asp	Ala	Pro
	290					295					300				
Cys	Ser	Leu	Pro	Ala	Glu	Ala	Ala	Leu	Cys	Trp	Arg	Ala	Pro	Gly	Gly
305					310					315					320
Asp	Pro	Cys	Gln	Pro	Leu	Val	Pro	Pro	Leu	Ser	Trp	Glu	Asn	Val	Thr
			325						330					335	
Val	Asp	Val	Asn	Ser	Ser	Glu	Lys	Leu	Gln	Leu	Gln	Glu	Cys	Leu	Trp
			340					345					350		

Ala	Asp	Ser	Leu	Gly	Pro	Leu	Lys	Asp	Asp	Val	Leu	Leu	Leu	Glu	Thr
	355						360				365				
Arg	Gly	Pro	Gln	Asp	Asn	Arg	Ser	Leu	Cys	Ala	Leu	Glu	Pro	Ser	Gly
	370					375					380				
Cys	Thr	Ser	Leu	Pro	Ser	Lys	Ala	Ser	Thr	Arg	Ala	Ala	Arg	Leu	Gly
385					390					395				400	
Glu	Tyr	Leu	Leu	Gln	Asp	Leu	Gln	Ser	Gly	Gln	Cys	Leu	Gln	Leu	Trp
			405					410					415		
Asp	Asp	Asp	Leu	Gly	Ala	Leu	Trp	Ala	Cys	Pro	Met	Asp	Lys	Tyr	Ile
			420					425					430		
His	Lys	Arg	Trp	Ala	Leu	Val	Trp	Leu	Ala	Cys	Leu	Leu	Phe	Ala	Ala
	435						440					445			
Ala	Leu	Ser	Leu	Ile	Leu	Leu	Leu	Lys	Lys	Asp	His	Ala	Lys	Gly	Trp
	450					455					460				
Leu	Arg	Leu	Leu	Lys	Gln	Asp	Val	Arg	Ser	Gly	Ala	Ala	Ala	Arg	Gly
465					470					475				480	
Arg	Ala	Ala	Leu	Leu	Tyr	Ser	Ala	Asp	Asp	Ser	Gly	Phe	Glu	Arg	
			485					490					495		
Leu	Val	Gly	Ala	Leu	Ala	Ser	Ala	Leu	Cys	Gln	Leu	Pro	Leu	Arg	Val
			500					505					510		
Ala	Val	Asp	Leu	Trp	Ser	Arg	Arg	Glu	Leu	Ser	Ala	Gln	Gly	Pro	Val
	515						520					525			
Ala	Trp	Phe	His	Ala	Gln	Arg	Arg	Gln	Thr	Leu	Gln	Glu	Gly	Gly	Val
	530					535					540				
Val	Val	Leu	Leu	Phe	Ser	Pro	Gly	Ala	Val	Ala	Leu	Cys	Ser	Glu	Trp
545					550					555				560	
Leu	Gln	Asp	Gly	Val	Ser	Gly	Pro	Gly	Ala	His	Gly	Pro	His	Asp	Ala
			565					570						575	
Phe	Arg	Ala	Ser	Leu	Ser	Cys	Val	Leu	Pro	Asp	Phe	Leu	Gln	Gly	Arg
			580					585					590		
Ala	Pro	Gly	Ser	Tyr	Val	Gly	Ala	Cys	Phe	Asp	Arg	Leu	Leu	His	Pro
	595						600					605			
Asp	Ala	Val	Pro	Ala	Leu	Phe	Arg	Thr	Val	Pro	Val	Phe	Thr	Leu	Pro
	610					615						620			
Ser	Gln	Leu	Pro	Asp	Phe	Leu	Gly	Ala	Leu	Gln	Gln	Pro	Arg	Ala	Pro
625					630					635				640	
Arg	Ser	Gly	Arg	Leu	Gln	Glu	Arg	Ala	Glu	Gln	Val	Ser	Arg	Ala	Leu
			645						650					655	
Gln	Pro	Ala	Leu	Asp	Ser	Tyr	Phe	His	Pro	Pro	Gly	Thr	Pro	Ala	Pro
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<210> 11
 <211> 705
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Chimeric Zcytor14 protein.

<400> 11

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 Cys Ser Pro Gly Leu Ser Cys Arg Leu Trp Asp Ser Asp Ile Leu Cys
 35 40 45
 Leu Pro Gly Asp Ile Val Pro Ala Pro Gly Pro Val Leu Ala Pro Thr
 50 55 60
 His Leu Gln Thr Glu Leu Val Leu Arg Cys Gln Lys Glu Thr Asp Cys
 65 70 75 80
 Asp Leu Cys Leu Arg Val Ala Val His Leu Ala Val His Gly His Trp
 85 90 95
 Glu Glu Pro Glu Asp Glu Glu Lys Phe Gly Gly Ala Ala Asp Ser Gly
 100 105 110
 Val Glu Glu Pro Arg Asn Ala Ser Leu Gln Ala Gln Val Val Leu Ser
 115 120 125
 Phe Gln Ala Tyr Pro Thr Ala Arg Cys Val Leu Leu Glu Val Gln Val
 130 135 140
 Pro Ala Ala Leu Val Gln Phe Gly Gln Ser Val Gly Ser Val Val Tyr
 145 150 155 160
 Asp Cys Phe Glu Ala Ala Leu Gly Ser Glu Val Arg Ile Trp Ser Tyr
 165 170 175
 Thr Gln Pro Arg Tyr Glu Lys Glu Leu Asn His Thr Gln Gln Leu Pro
 180 185 190
 Ala Leu Pro Trp Leu Asn Val Ser Ala Asp Gly Asp Asn Val His Leu
 195 200 205
 Val Leu Asn Val Ser Glu Glu Gln His Phe Gly Leu Ser Leu Tyr Trp
 210 215 220
 Asn Gln Val Gln Gly Pro Pro Lys Pro Arg Trp His Lys Asn Leu Thr
 225 230 235 240
 Gly Pro Gln Ile Ile Thr Leu Asn His Thr Asp Leu Val Pro Cys Leu
 245 250 255
 Cys Ile Gln Val Trp Pro Leu Glu Pro Asp Ser Val Arg Thr Asn Ile
 260 265 270

AI
 cont

Cys Pro Phe Arg Glu Asp Pro Arg Ala His Gln Asn Leu Trp Gln Ala
 275 280 285
 Ala Arg Leu Arg Leu Leu Thr Leu Gln Ser Trp Leu Leu Asp Ala Pro
 290 295 300
 Cys Ser Leu Pro Ala Glu Ala Ala Leu Cys Trp Arg Ala Pro Gly Gly
 305 310 315 320
 Asp Pro Cys Gln Pro Leu Val Pro Pro Leu Ser Trp Glu Asn Val Thr
 325 330 335
 Val Asp Lys Val Leu Glu Phe Pro Leu Leu Lys Gly His Pro Asn Leu
 340 345 350
 Cys Val Gln Val Asn Ser Ser Glu Lys Leu Gln Leu Gln Glu Cys Leu
 355 360 365
 Trp Ala Asp Ser Leu Gly Pro Leu Lys Asp Asp Val Leu Leu Leu Glu
 370 375 380
 Thr Arg Gly Pro Gln Asp Asn Arg Ser Leu Cys Ala Leu Glu Pro Ser
 385 390 395 400
 Gly Cys Thr Ser Leu Pro Ser Lys Ala Ser Thr Arg Ala Ala Arg Leu
 405 410 415
 Gly Glu Tyr Leu Leu Gln Asp Leu Gln Ser Gly Gln Cys Leu Gln Leu
 420 425 430
 Trp Asp Asp Asp Leu Gly Ala Leu Trp Ala Cys Pro Met Asp Lys Tyr
 435 440 445
 Ile His Lys Arg Trp Ala Leu Val Trp Leu Ala Cys Leu Leu Phe Ala
 450 455 460
 Ala Ala Leu Ser Leu Ile Leu Leu Leu Lys Lys Asp His Ala Lys Gly
 465 470 475 480
 Trp Leu Arg Leu Leu Lys Gln Asp Val Arg Ser Gly Ala Ala Ala Arg
 485 490 495
 Gly Arg Ala Ala Leu Leu Leu Tyr Ser Ala Asp Asp Ser Gly Phe Glu
 500 505 510
 Arg Leu Val Gly Ala Leu Ala Ser Ala Leu Cys Gln Leu Pro Leu Arg
 515 520 525
 Val Ala Val Asp Leu Trp Ser Arg Arg Glu Leu Ser Ala Gln Gly Pro
 530 535 540
 Val Ala Trp Phe His Ala Gln Arg Arg Gln Thr Leu Gln Glu Gly Gly
 545 550 555 560
 Val Val Val Leu Leu Phe Ser Pro Gly Ala Val Ala Leu Cys Ser Glu
 565 570 575
 Trp Leu Gln Asp Gly Val Ser Gly Pro Gly Ala His Gly Pro His Asp
 580 585 590
 Ala Phe Arg Ala Ser Leu Ser Cys Val Leu Pro Asp Phe Leu Gln Gly
 595 600 605

AI
conf.

Arg Ala Pro Gly Ser Tyr Val Gly Ala Cys Phe Asp Arg Leu Leu His
 610 615 620
 Pro Asp Ala Val Pro Ala Leu Phe Arg Thr Val Pro Val Phe Thr Leu
 625 630 635 640
 Pro Ser Gln Leu Pro Asp Phe Leu Gly Ala Leu Gln Gln Pro Arg Ala
 645 650 655
 Pro Arg Ser Gly Arg Leu Gln Glu Arg Ala Glu Gln Val Ser Arg Ala
 660 665 670
 Leu Gln Pro Ala Leu Asp Ser Tyr Phe His Pro Pro Gly Thr Pro Ala
 675 680 685
 Pro Gly Arg Gly Val Gly Pro Gly Ala Gly Pro Gly Ala Gly Asp Gly
 690 695 700
 Thr
 705

<210> 12
 <211> 675
 <212> PRT
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 Cys Ser Pro Gly Leu Ser Cys Arg Leu Trp Asp Ser Asp Ile Leu Cys
 35 40 45
 Leu Pro Gly Asp Ile Val Pro Ala Pro Gly Pro Val Leu Ala Pro Thr
 50 55 60
 His Leu Gln Thr Glu Leu Val Leu Arg Cys Gln Lys Glu Thr Asp Cys
 65 70 75 80
 Asp Leu Cys Leu Arg Val Ala Val His Leu Ala Val His Gly His Trp
 85 90 95
 Glu Glu Pro Glu Asp Glu Glu Lys Phe Gly Gly Ala Ala Asp Ser Gly
 100 105 110
 Val Glu Glu Pro Arg Asn Ala Ser Leu Gln Ala Gln Val Val Leu Ser
 115 120 125
 Phe Gln Ala Tyr Pro Thr Ala Arg Cys Val Leu Leu Glu Val Gln Val
 130 135 140

A1
 cont.

Pro Ala Ala Leu Val Gln Phe Gly Gln Ser Val Gly Ser Val Val Tyr
 145 150 155 160
 Asp Cys Phe Glu Ala Ala Leu Gly Ser Glu Val Arg Ile Trp Ser Tyr
 165 170 175
 Thr Gln Pro Arg Tyr Glu Lys Glu Leu Asn His Thr Gln Gln Leu Pro
 180 185 190
 Ala Leu Pro Trp Leu Asn Val Ser Ala Asp Gly Asp Asn Val His Leu
 195 200 205
 Val Leu Asn Val Ser Glu Glu Gln His Phe Gly Leu Ser Leu Tyr Trp
 210 215 220
 Asn Gln Val Gln Gly Pro Pro Lys Pro Arg Trp His Lys Asn Leu Thr
 225 230 235 240
 Gly Pro Gln Ile Ile Thr Leu Asn His Thr Asp Leu Val Pro Cys Leu
 245 250 255
 Cys Ile Gln Val Trp Pro Leu Glu Pro Asp Ser Val Arg Thr Asn Ile
 260 265 270
 Cys Pro Phe Arg Glu Asp Pro Arg Ala His Gln Asn Leu Trp Gln Ala
 275 280 285
 Ala Arg Leu Arg Leu Leu Thr Leu Gln Ser Trp Leu Leu Asp Ala Pro
 290 295 300
 Cys Ser Leu Pro Ala Glu Ala Ala Leu Cys Trp Arg Ala Pro Gly Gly
 305 310 315 320
 Asp Pro Cys Gln Pro Leu Val Pro Pro Leu Ser Trp Glu Asn Val Thr
 325 330 335
 Val Asp Val Asn Ser Ser Glu Lys Leu Gln Leu Gln Glu Cys Leu Trp
 340 345 350
 Ala Asp Ser Leu Gly Pro Leu Lys Asp Asp Val Leu Leu Leu Glu Thr
 355 360 365
 Arg Gly Pro Gln Asp Asn Arg Ser Leu Cys Ala Leu Glu Pro Ser Gly
 370 375 380
 Cys Thr Ser Leu Pro Ser Lys Ala Ser Thr Arg Ala Ala Arg Leu Gly
 385 390 395 400
 Glu Tyr Leu Leu Gln Asp Leu Gln Ser Gly Gln Cys Leu Gln Leu Trp
 405 410 415
 Asp Asp Asp Leu Gly Ala Leu Trp Ala Cys Pro Met Asp Lys Tyr Ile
 420 425 430
 His Lys Arg Trp Ala Leu Val Trp Leu Ala Cys Leu Leu Phe Ala Ala
 435 440 445
 Ala Leu Ser Leu Ile Leu Leu Leu Lys Lys Asp His Ala Lys Ala Ala
 450 455 460
 Ala Arg Gly Arg Ala Ala Leu Leu Leu Tyr Ser Ala Asp Asp Ser Gly
 465 470 475 480

A1
 cont.

Phe Glu Arg Leu Val Gly Ala Leu Ala Ser Ala Leu Cys Gln Leu Pro
 485 490 495
 Leu Arg Val Ala Val Asp Leu Trp Ser Arg Arg Glu Leu Ser Ala Gln
 500 505 510
 Gly Pro Val Ala Trp Phe His Ala Gln Arg Arg Gln Thr Leu Gln Glu
 515 520 525
 Gly Gly Val Val Val Leu Leu Phe Ser Pro Gly Ala Val Ala Leu Cys
 530 535 540
 Ser Glu Trp Leu Gln Asp Gly Val Ser Gly Pro Gly Ala His Gly Pro
 545 550 555 560
 His Asp Ala Phe Arg Ala Ser Leu Ser Cys Val Leu Pro Asp Phe Leu
 565 570 575
 Gln Gly Arg Ala Pro Gly Ser Tyr Val Gly Ala Cys Phe Asp Arg Leu
 580 585 590
 Leu His Pro Asp Ala Val Pro Ala Leu Phe Arg Thr Val Pro Val Phe
 595 600 605
 Thr Leu Pro Ser Gln Leu Pro Asp Phe Leu Gly Ala Leu Gln Gln Pro
 610 615 620
 Arg Ala Pro Arg Ser Gly Arg Leu Gln Glu Arg Ala Glu Gln Val Ser
 625 630 635 640
 Arg Ala Leu Gln Pro Ala Leu Asp Ser Tyr Phe His Pro Pro Gly Thr
 645 650 655
 Pro Ala Pro Gly Arg Gly Val Gly Pro Gly Ala Gly Pro Gly Ala Gly
 660 665 670
 Asp Gly Thr
 675

A1
 cont.